

#### Sequence Listing

<110> Chen, Jian Goddard, Audrey Gurney, Austin L. Hillan, Kenneth Pennica, Diane Wood, William I. Yuan, Jean RECEIVED

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TECH CENTER 1600/2900

<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

<130> P1618P2C2

<140> US 09/904,553

<141> 2001-07-13

<150> US 09/665,350

<151> 2000-09-18

<150> PCT/US00/04414

<151> 2000-02-22

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<151> 1998-09-10

<150> US 60/062,285

<151> 1997-10-17

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gaagacactg aaagtgtgct gctctccagg aacctacggt cccgactgtc 550 Page 1

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Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Page 2

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Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu 50 55 60

Gly Lys Met Ala Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln 65 70 75

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Trp Gln Ala Gly Gln Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Page 5

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140 145 150
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155 160 165
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170 175 180
 Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg
185 190 195
 Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His Cys Glu 200 205 210
 Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys Val 215 220 225
 Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn 230 235
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr
245 250 255
 Cys Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly 260 265 270
 Glu Gln Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly 285
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Asp Cys Ala Leu Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu
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Phe Cys Asn Arg Thr Val Ser Asp Cys Cys Pro Asp Phe Trp Asp 80 85 90
Phe Cys Leu Gly Val Pro Pro Pro Phe Pro Pro Ile Gln Gly Cys
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125 130 135
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 <213> Homo Sapien
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<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;223> Synthetic Oligonucleotide Probe

<sup>&</sup>lt;210> 20

<sup>&</sup>lt;211> 24

<sup>&</sup>lt;212> DNA

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  gtgagggacc agggcgccat gaccgaccag ctgagcaggc ggcagatccg 150
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Page 16

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Asn Gln Leu Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser 300  Asn Leu Lys Gln Leu Thr Ala Arg Asn 310 Pro Trp Phe Cys 3915  Cys Ser Ile Lys Trp Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser 320  Ser Leu Asn Val Arg Gly Phe Met Cys Gln Gly Pro Glu Gln Val 345  Arg Gly Met Ala Val Arg Glu Leu Asn Met Asn Leu Leu Ser Cys 660  Pro Thr Thr Thr Pro Glu Leu Pro Leu Pro Thr Pro Ala Pro Ser 375  Thr Ala Ser Pro Thr Thr Gln Pro Pro Thr Pro Hor Ser 1860  Pro Ser Arg Ser Tyr Thr Pro Pro Pro Thr Pro Thr Thr Ser Lys Leu Asn Asp Pro Thr Ile Pro Asp 395  Pro Thr Ile Pro Asp Gly Arg Glu Arg Val Thr Pro Pro Asp 600  Pro Thr Ile Pro Asp Trp Leu Ser Leu Pro Leu Pro Val Asn Asp Pro Thr Asp 610 Pro Thr Pro Val Asn Asp Thr Asp 610 Pro Thr Pro Val Asn Asp 745  Ser Ile Gln Val Ser Trp Leu Ser Leu Pro Val Met Ala Tys 1860  Lys Leu Thr Trp Val												•		9	
Sor Ile Lys Trp Val Thr Glu Trp Leu Ser Ile Wals Pro Val Thr Pro Pro Val Ser Ile Gln Asn Leu Glu Asn Asn Asn Asn Has Ser Ile Gln Val Ser Ile Gln Val Ser Ile Gln Asn Leu Glu Asn Asn Leu Glu Asn Asn Leu Glu Asn Asn Asn Leu Glu Asn Asn Asn Ile Glu Asn Asn Leu Glu Ser Asn Ile Pro Asn Asn Asn Ile Asn Asn Asn Ile Asn	Asn	Gln	Leu	Arg	Met 290	Leu	Thr	Gln	Gly	val 295	Phe	Asp	Asn	Leu	
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65 70 75 Val Lys Glu Phe Ile Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val Gly Leu Leu Gln Tyr Gly Ser Thr Val 105 Lys Asn Glu Phe Ser Leu Lys Thr Phe Lys Arg Lys Ser Glu Val 110 115 120 120 Glu Arg Ala Val Lys Arg Met Arg His Leu Ser Thr Gly Thr Met 125 130 135 Thr Gly Leu Ala Ile Gln Tyr Ala Leu Asn Ile Ala Phe Ser Glu 140 145 150 Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn Val Pro Arg Val Ile 155 160 165 Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser Val Ala Glu Val 170 175 180 Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe Ala Ile Gly 185 190 195 Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly Ser Glu 200 205 210 Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln Ile

P1618P2C2 sequence listing.txt
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230 235 240 Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn 245 250 255 Ile Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu 260 265 270 Asn Ser Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met 275 280 285 Glu Asp His Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser 290 295 300 Phe Val Cys Gln Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly 305 310 315 Lys Arg Cys Val Ala Val Asp Tyr Cys Ala Ser Glu Asn His Gly 320 325 330 Cys Glu His Glu Cys Val Asn Ala Asp Gly Ser Tyr Leu Cys Gln 335 340 345 Cys His Glu Gly Phe Ala Leu Asn Pro Asp Glu Lys Thr Cys Thr 350 355 360 Arg Ile Asn Tyr Cys Ala Leu Asn Lys Pro Gly Cys Glu His Glu 365 370 375 Cys Val Asn Met Glu Glu Ser Tyr Tyr Cys Arg Cys His Arg Gly 380 385 390 Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys Ser Arg Val Asp His 395 400 405 405 Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu Cys Leu Asn Thr 410 415 420 420 Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe Leu Ile Asn 425 430 435 435 Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu Leu Ser 440 445 450 Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser Phe 455 460 465 Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys
470 475 480 Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys 485 490 495 Glu His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys 500 505 510 Phe Glu Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg 515 520 525 Lys Asp Val Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys 530 535 540

P1618P2C2 sequence listing.txt Val Asn Ser Asp Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp Gly Lys Arg Cys Arg Arg Lys Asp Val 560 565 Lys Ser Thr His His Gly Cys Glu His Ile Cys Val Asn Asn Gly
575 580 585 580 Asn Ser Tyr Ile Cys Lys Cys Ser Glu Gly Phe Val Leu Ala Glu 590 595 600 Asp Gly Arg Arg Cys Lys Lys Cys Thr Glu Gly Pro Ile Asp Leu
605 610 Val Phe Val Ile Asp Gly Ser Lys Ser Leu Gly Glu Glu Asn Phe 620 625 630 Glu Val Val Lys Gln Phe Val Thr Gly Ile Ile Asp Ser Leu Thr 640 645 Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu Gln Tyr Ser Thr 650 655 660 Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly Lys Gly 680 685 690 Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser Phe 695 700 705 Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
710 715 720 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser 725 730 735 Glu Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala 740 745 750 750 Val Gly Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala 755 760 765 Ser Glu Pro Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser 770 775 780 Thr Met Asp Glu Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu 785 790 795 795 Ala Leu Glu Asp Ser Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu 800 805 810 810 Leu Pro Lys Thr Val Gln Gln Pro Thr Glu Ser Glu Pro Val Thr 815 825 Ile Asn Ile Gln Asp Leu Leu Ser Cys Ser Asn Phe Ala Val Gln 830 835 840 His Arg Tyr Leu Phe Glu Glu Asp Asn Leu Leu Arg Ser Thr Gln 845 850 855

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Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu 260 265 270

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Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser

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P1618P2C2 sequence listing.txt 295
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  Arg Leu Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro
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$$50$$
  $55$   $60$ 

<sup>&</sup>lt;210> 49

<sup>&</sup>lt;211> 690

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

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Thr Asn Thr Glu Gly Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe 80 85 90

P1618P2C2 sequence listin	g.txt
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Ile Lys Glu Pro Val Ala Leu Leu Gln Glu Val Tyr Arg	Asn Ser
140 145	150
Val Thr Asp Leu Ser Pro Thr Asp Ile Ile Thr Tyr Ile	Glu Ile
155 160	165
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170 175	180
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185 190	195
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245 250	255
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350 355	360
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365 370	375
Ser Pro Asp Thr Met Asn Gly Ser Trp Ser Ser Glu Gly C	ys Glu
380 385	390
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P1618P2C2 sequence listing_txt
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   Ile Lys Asp Tyr Asm Ile Leu Thr Arg Ile Thr Gln Leu Gly Ile
                   425
                                        430
  Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr Phe Trp
440 445 450
  Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys Asn
  Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
  Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly
  Leu Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile
  Glu Gly Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn
                   515
                                        520
  Lys Gly Phe Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser
                                                            540
  Pro Ala Val Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg
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  Tyr Gly Thr Thr Lys Val Cys Trp Leu Ser Thr Glu Asn Asn Phe
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  Ile Trp Ser Phe Ile Gly Pro Ala Cys Leu Ile Ile Leu Val Asn
                                       580
                                                            585
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590 595 600
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                  635
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 aacttcttat tgaaacctca aaattatgat aattctgaag aggaggaaag 200
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 tatatgaact tgaaaaaata acatttacat taagtcatcg aaaggtcaca 300
 gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat 350
 gaatggcagc tggtcttcag agggctgtga gctgacatac tcaaatgaga 400
 cccacacctc atgccgctgt aatcacctga cacattttgc aattttgatg 450
 tcctctggtc cttccattgg tattaaagat tataatattc ttacaaggat 500
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tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa tgctcgggtg 250
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tgctgtgtgg aagcagcggg ggaagaccta gaaccctttc cccagcactt 2000 ggttttccaa catgatattt atgagtaatt tattttgata tgtacatctc 2050 ttattttctt acattattta tgcccccaaa ttatatttat gtatgtaagt 2100 gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

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<400> 59

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$$110$$
  $115$   $120$ 

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<sup>&</sup>lt;213> Homo Sapien

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<400> 62
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agccgccacc gcctcctcct gctgctgctg cgctacctgg tggtcgccct 150
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tgtcaagaca aagaagggaa tccagctcct gaatacacat ggtttaagga 600
tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca 650
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<211> 312 <212> PRT

<213> Homo Sapien

<400> 64

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Ala Ile Leu Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg 50 55 60

Leu Glu Trp Lys Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr
65 70 75

Gln Gln Thr Leu Gln Gly Asp Phe Lys Asn Arg Ala Glu Met Ile 80 85 90

Asp Phe Asn Ile Arg Ile Lys Asn Val Thr Arg Ser Asp Ala Gly
95 100 105

Lys Tyr Arg Cys Glu Val Ser Ala Pro Ser Glu Gln Gly Gln Asn 110 115 120

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Val Glu Leu Arg Cys Gln Asp Lys Glu Gly Asn Pro Ala Pro Glu 155 160 165 Page 39

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 Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp Thr
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 Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
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 Leu Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu
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tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

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Il	е ту	r Me	t Gl	u Al 5	a se O	r Th	r Va	l As	р су: 5:	s Asr 5	ızA r	) Lei	ı Gl	y Leu 60
Lei	u Th	r Ph	e Pr	o Al 6	a Ar	g Lei	ı Pro	o Al	a Ası 70		- Glr	ılle	e Lei	Leu 75
Lei	u Gl	n Th	r As	n Ası 80	n Ilo O	e Ala	a Lys	s Il	e Glu 85		Ser	Thi	- Ast	Phe 90
Pro	o Va	l As	n Le	u Thi	r Gly	y Leu	ı Asp	) Le	ser 100	Gln	Asņ	ı Asr	ı Lei	ser 105
Ser	' Va	l Th	r Ası	n Ile 110	e Asr	י ∨al	Lys	Lys	5 Met 115	Pro	Gln	Leu	l Lei	Ser 120
۷a٦	Туі	r Le	u Gli	ม Gไเ 125	ı Asr	ı Lys	Leu	Thr	Glu 130	Leu	Pro	Glu	Lys	Cys 135
Leu	sei	G]	u Lei	Ser 140	Asr	Leu	Gln	Glu	Leu 145	Tyr	Ile	Asn	His	Asn 150
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Glu	Ile	Pro	Asp	Asn 230	Ala	Leu	۷al	Gly	Leu 235	Glu	Asn	Leu	Glu	Ser 240
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Leu	Gln	Lys	Val	Va1 260	Asn	Leu	Lys	Phe	Leu 265	Asp	Leu	Asn	Lys	Asn 270
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Leu	Lys	Glu	Leu	G]y 290	Ile	Asn	Asn	Met	Pro 295	Glu	Leu	Ile	Ser	Ile 300
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Phe	Arg	Leu	Pro	Lys 335	Leu	Glu	Ser	Leu	Met 340	Leu .	Asn	Ser		Ala 345
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P1618P2C2 sequence listing.txt
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                                          430
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485
490
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530 535 540
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560 565 570
Ile Pro Ser Asp Val Lys Val Tyr Asn Leu Thr His Leu Asn Pro
Ser Thr Glu Tyr Lys Ile Cys Ile Asp Ile Pro Thr Ile Tyr Gln
590 595 600
Lys Asn Arg Lys Lys Cys Val Asn Val Thr Thr Lys Gly Leu His
605 610 615
Pro Asp Gln Lys Glu Tyr Glu Lys Asn Asn Thr Thr Leu Met
Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile Gly Val Ile Cys Leu 645
Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp Gly Gly His Ser 650 655 660
Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala Leu Gly Glu
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P1618P2C2 sequence listing.txt 665 Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro Thr Asn Met Ser <210> 70 <211> 1305 <212> DNA <213> Homo Sapien <400> 70 gcccgggact ggcgcaaggt gcccaagcaa ggaaagaaat aatgaagaga 50 cacatgtgtt agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag 100 tgtggacagg gctggaacct ttaccacgct tgttggagta gatgaggaat 150 gggctcgtga ttatgctgac attccagcat gaatctggta gacctgtggt 200 taacccgttc cctctccatg tgtctcctcc tacaaagttt tgttcttatg 250 atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300 ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa 350 tacctagaga tetteetet gaaacagtet tactgtatet ggaetecaat 400 cagatcacat ctattcccaa tgaaattttt aaggacctcc atcaactgag 450 agttctcaac ctgtccaaaa atggcattga gtttatcgat gagcatgcct 500 tcaaaggagt agctgaaacc ttgcagactc tggacttgtc cgacaatcgg 550 attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600 aattgccaac aacccctggc actgcgactg tactctacag caagttctga 650 ggagcatggc gtccaatcat gagacagccc acaacgtgat ctgtaaaacg 700 tccgtgttgg atgaacatgc tggcagacca ttcctcaatg ctgccaacga 750 cgctgacctt\_tgtaacctcc\_ctaaaaaaac\_taccgattat\_gccatgctgg\_800 tcaccatgtt tggctggttc actatggtga tctcatatgt ggtatattat 850 gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900 cctgccaagc aggcagaaga aagcagatga acctgatgat attagcactg 950 tggtatagtg tccaaactga ctgtcattga gaaagaaaga aagtagtttg 1000 cgattgcagt agaaataagt ggtttacttc tcccatccat tgtaaacatt 1050

tgaaactttg tatttcagtt ttttttgaat tatgccactg ctgaactttt 1100 aacaaacact acaacataaa taatttgagt ttaggtgatc caccccttaa 1150

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<212> PRT

<213> Homo Sapien

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Arg Val Leu Asn Leu Ser Lys Asn Gly Ile Glu Phe Ile Asp Glu 95 100 105

His Ala Phe Lys Gly Val Ala Glu Thr Leu Gln Thr Leu Asp Leu
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Cys Thr Leu Gln Gln Val Leu Arg Ser Met Ala Ser Asn His Glu 155 160 165

Thr Ala His Asn Val Ile Cys Lys Thr Ser Val Leu Asp Glu His 170 175 180

Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala Asp Leu Cys 185 190 195

Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val Thr Met 200 205 210

Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr Val 215 220 225

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Leu Asp Leu Gly Lys Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu 80 85 90

Page 48

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525

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Gln	Ile	Lys	Ile	Arg 320	Pro	Thr	Ala		Ile 325	Ala	Thr	Gly	Ser	Ser 330
Arg	Asn	Lys	Pro		Ala	Asn	Ser			Cys	Pro	Glу	Gly	
Ser	Cys	Asp	His	11e 350	Pro	Gly	Ser	Gly	Leu 355	Lys	Met	Asn	Cys	Asn 360
Asn	Arg	Asn	٧a٦	Ser 365	Ser	Leu	Ala	Asp	Leu 370	Lys	Pro	Lys	Leu	Ser 375
Asn	val	Gln	Glu	Leu 380	Phe	Leu	Arg	Asp	Asn 385	Lys	Ile	His	Ser	Ile 390
Arg	Lys	Ser	His	Phe 395	val	Asp	Tyr	Lys	400	Leu ge 58		Leu	Leu	Asp 405
											•			

										,			J	. •
Leu	ı Gly	⁄ Asn	Asn	410	ılle	Ala	Thr	· val	Glu 415		Asn	Thr	Phe	Lys 420
Asr	1 Leu	Leu	Asp	Leu 425	Arg	Trp	Leu	ı Tyr	Met 430		Ser	Asn	Tyr	Leu 435
Asp	Thr	Leu	Ser	Arg 440	Glu	Lys	Phe	Ala	Gly 445	Leu	Gln	Asn	Leu	G]u 450
Tyr	Leu	Asn	Val	G]u 455	Tyr	Asn	Ala	Ile	G]n 460		Ile	Leu	Pro	Gly 465
Thr	Phe	Asn	Ala	Met 470	Pro	Lys	Leu	Arg	11e 475	Leu	Ile	Leu	Asn	Asn 480
Asn	Leu	Leu	Arg	Ser 485	Leu	Pro	٧a٦	Asp	Va1 490	Phe	Ala	Gly	۷al	Ser 495
Leu	Ser	Lys	Leu	Ser 500	Leu	ніѕ	Asn	Asn	Tyr 505	Phe	Met	Tyr	Leu	Pro 510
۷a٦	Ala	Gly	val	Leu 515	Asp	Gln	Leu	Thr	Ser 520	Ile	Ile	Gln	IJе	Asp 525
Leu	His	Gly	Asn	Pro 530	Trp	Glu	Cys	Ser	Cys 535	Thr	Ile	۷al	Pro	Phe 540
Lys	Gln	Trp	Ala	G1u 545	Arg	Leu	Gly	Ser	G]u 550	val	Leu	Met	Ser	Asp 555
Leu	Lys	Cys	Glu	Thr 560	Pro	Val	Asn	Phe	Phe 565	Arg	Lys	Asp	Phe	Met 570
Leu	Leu	Ser	Asn	Asp 575	Glu	Ile	Cys	Pro	G]n 580	Leu	Tyr	Ala	Arg	11e 585
Ser	Pro	Thr	Leu	Thr 590	Ser	His	Ser	Lys	Asn 595	Ser	Thr	Gly	Leu	Ala 600
Glu	Thr	Gly	Thr	His 605	Ser	Asn	Ser	Tyr	Leu 610	Asp	Thr	Ser	Arg	Val 615
Ser	Ile	Ser	٧a٦	Leu 620	۷a٦	Pro	Gly	Leu	Leu 625	Leu	٧a٦	Phe	٧a٦	Thr 630
Ser	Ala	Phe	Thr	va1 635	Val	Gly	Met	Leu	Va1 640	Phe	Ile	Leu	Arg	Asn 645
Arg	Lys	Arg	Ser	Lys 650	Arg	Arg	Asp	Ala	Asn 655	Ser	Ser	Ala	Ser	G]u 660
Ile	Asn	Ser	Leu	G]n 665	Thr	val	Cys	Asp	Ser 670	Ser	Tyr	Trp	His	Asn 675
Gly	Pro	Tyr	Asn	Ala 680	Asp	Gly	Аlа	His	Arg 685	۷a٦	Tyr	Asp	Cys	G]y 690
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P1618P2C2 sequence listing.txt
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140 145 150 Gly Val Glu Pro Ala Gly Trp Lys Glu Met Arg Cys His Leu Arg 165 Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu Val Leu Cys Pro 170 175 180 Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr Arg Ala Pro 185 190 195 Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro Gly Thr 205 Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val Thr 215 220 225 Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly 230 235 240 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys 255 Cys Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala 260 265 270 Cys Glu Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser 275 280 285 Page 62

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Cys Val Thr Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly
290 295 300
                                                           300
                                      295
 Val Pro Thr Arg Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro
 Gln Arg Thr Trp Pro Ile Arg Val Asp Glu Lys Leu Gly Glu Thr
 Pro Leu Val Pro Glu Gln Asp Asn Ser Val Thr Ser Ile Pro Glu
                                      340
 Ile Pro Arg Trp Gly Ser Gln Ser Thr Met Ser Thr Leu Gln Met 350 355 360
 Ser Leu Gln Ala Glu Ser Lys Ala Thr Ile Thr Pro Ser Gly
 Val Ile Ser Lys Phe Asn Ser Thr Thr Ser Ser Ala Thr Pro Gln
                                      385
 Ala Phe Asp Ser Ser Ser Ala Val Val Phe Ile Phe Val Ser Thr
                                                           405
                                      400
 Ala Val Val Leu Val Ile Leu Thr Met Thr Val Leu Gly Leu
                                                           420
                 410
 Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln Pro Arg Lys
                                      430
 Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu Pro Ala
                                      445
                                                           450
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                                      460
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  ggcgtgtgtg ccggcgcgcg cgccgtgggg tgcaaacccc gagcgtctac 300
                                        Page 64
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<211> 415

<212> PRT

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<400> 104

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Phe Thr Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly 35 40 45

Ser Glu Gly Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr 50 55 60

Trp Lys Ile Thr Val Pro Glu Gly Lys Val Val Leu Asn Phe 65 70 75

Arg Phe Ile Asp Leu Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe 80 85 90

Val Asp Val Tyr Asn Gly His Ala Asn Gly Gln Arg Ile Gly Arg 95 100 105

Phe Cys Gly Thr Phe Arg Pro Gly Ala Leu Val Ser Ser Gly Asn 110 115 120

Lys Met Met Val Gln Met Ile Ser Asp Ala Asn Thr Ala Gly Asn 125 130 135

Gly Phe Met Ala Met Phe Ser Ala Ala Glu Pro Asn Glu Arg Gly 140 145 150

Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg Pro Ser Gly Ser Phe 155 160 165

Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro Ala Gly Val Thr 170 175 180

Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu Ile Glu Leu 185 190 195

Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys Arg Tyr 200 205 210

Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala Arg 215 220 225

Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Page 66

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P1618P2C2 sequence listing.txt
                  245
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                                                             285
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 Cys Arg Arg Thr Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp
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 Phe Val Leu Ala Gly Thr Val Ile Thr Thr Ile Thr Arg Asp Gly 320 325 330
 Ser Leu His Ala Thr Val Ser Ile Ile Asn Ile Tyr Lys Glu Gly
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                                        340
 Asn Leu Ala Ile Gln Gln Ala Gly Lys Asn Met Ser Ala Arg
 Thr Val Val Cys Lys Gln Cys Pro Leu Leu Arg Arg Gly Leu Asn 365 370 375
                                                             375
 Tyr Ile Ile Met Gly Gln Val Gly Glu Asp Gly Arg Gly Lys Ile
380 385 390
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                                        400
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P1618P2C2 sequence listing.txt tgactggcta ctggttgtca gagcgcagtg accgtgtgct ggagggcttc 1350 atcaagggca gataatcgcg gccaccacct gtaggacctc ctcccaccca 1400 cgctgccccc agagcttggg ctgccctcct gctggacact caggacagct 1450 tggtttattt ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500 gcccaggtac ccaggcccgg gcagacaagg cccctggggt aaaaagtagc 1550 cctgaaggtg gataccatga gctcttcacc tggcggggac tggcaggctt 1600 cacaatgtgt gaatttcaaa agtttttcct taatggtggc tgctagagct 1650 ttggcccctg cttaggatta ggtggtcctc acaggggtgg ggccatcaca 1700 gctccctcct gccagctgca tgctgccagt tcctgttctg tgttcaccac 1750 atccccacac cccattgcca cttatttatt catctcagga aataaagaaa 1800 ggtcttggaa agttaaaaaa aaaaaaaaa aaaaaaaa 1838

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65 70 75 Glu Glu Glu Asn Leu Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu 80 85 90 Val Glu Val Leu Glu Gly Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser Glu Glu Leu Val Glu Ser Trp Trp
110 115 120 Phe His Lys Gln Gln Glu Ala Pro Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro Ala Gly Thr Phe Gly Pro 140 145 Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu Arg Pro Cys Gly Gly 165 Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly Gly Ser Gly His 170 175 180 Page 69

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Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln Cys
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Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His Leu Val
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Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro Glu
215 220 225
Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His 230 235 240
Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn 245 250 255
Cys Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu
260 265 270
Cys Arg Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly 275 280 285
Pro Gly Arg Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val
290 295
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Ser Lys Cys Leu Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro
305 310 315
                                                                315
Gly Glu Asn Lys Gln Cys Glu Asn Thr Glu Gly Gly Tyr Arg
320 325
Ile Cys Ala Glu Gly Tyr Lys Gln Met Glu Gly Ile Cys Val Lys
335 340 345
Glu Gln Ile Pro Glu Ser Ala Gly Phe Phe Ser Glu Met Thr Glu
                  350
                                         355
                                                                360
Asp Glu Leu Val Val Leu Gln Gln Met Phe Phe Gly Ile Ile Ile
                  365
Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp Leu Val Phe Thr
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Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly Tyr Trp Leu
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Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys Gly Arg
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<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Synthetic Oligonucleotide Probe

<sup>&</sup>lt;400> 110

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 gtgttgcccc tggccagccc cggggccgcc ctgaccgggg agcagctcct 150
 gggcagcctg ctgcggcagc tgcagctcaa agaggtgccc accctggaca 200
 gggccgacat ggaggagctg gtcatcccca cccacgtgag ggcccagtac 250
 gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca 350
 gcacacacct gctggtgttc ggcatggagc agcggctgcc gcccaacagc 400
 gagctggtgc aggccgtgct gcggctcttc caggagccgg tccccaaggc 450
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 tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa ccgcacctcc 550
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 agccgctgct gctacaggtg tcggtgcaga gggagcatct gggcccgctg 700
 gcgtccggcg cccacaagct ggtccgcttt gcctcgcagg gggcgccagc 750
 cgggcttggg gagccccagc tggagctgca caccctggac cttggggact 800
  atggagetea gggegaetgt gaeeetgaag caeeaatgae egagggeaee 850
                                        Page 71
```

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cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900
cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg 950
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gggcctcgac agtgcatcgc ctcggagact gactcgctgc ccatgatcgt 1050
cagcatcaag gagggaggca ggaccaggcc ccaggtggtc agcctgccca 1100
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<sup>&</sup>lt;213> Homo Sapien

<sup>&</sup>lt;400> 114
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1 5 10 15

Ala Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser 20 25 30

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P1618P2C2 sequence listing.txt
Phe Gln Glu Pro Val Pro Lys Ala Ala Leu His Arg His Gly Arg
Leu Ser Pro Arg Ser Ala Arg Ala Arg Val Thr Val Glu Trp Leu
Arg Val Arg Asp Asp Gly Ser Asn Arg Thr Ser Leu Ile Asp Ser
155 160 165
Arg Leu Val Ser Val His Glu Ser Gly Trp Lys Ala Phe Asp Val
170 175 180
Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg Pro Arg Gln
                                                               195
                  185
                                        190
Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu Gly Pro
200 205 210
Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln Gly
215 220 225
Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala
245 250 255
Pro Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile
260 265 270
Asp Leu Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro
275 280 285
Pro Gly Phe Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro
290 295 300
Pro Glu Ala Leu Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln
                                                               315
Cys Ile Ala Ser Glu Thr Asp Ser Leu Pro Met Ile Val Ser Ile
Lys Glu Gly Gly Arg Thr Arg Pro Gln Val Val Ser Leu Pro Asn 335 340
Met Arg Val Gln Lys Cys Ser Cys Ala Ser Asp Gly Ala Leu Val
350 355 360
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Pro Arg Arg Leu Gln Pro 365

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<sup>&</sup>lt;211> 21

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Synthetic Oligonucleotide Probe

<sup>&</sup>lt;400> 115

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<sup>&</sup>lt;210> 116

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P1618P2C2 sequence listing.txt
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<223> Synthetic Oligonucleotide Probe
<400> 116
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<210> 117
<211> 45
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 117
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<210> 118
<211> 1857
<212> DNA
<213> Homo Sapien
<400> 118
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 tggcgatcct gttgtgctcc ctggcattgg gcagtgttac agtgcactct 150
 tctgaacctg aagtcagaat tcctgagaat aatcctgtga agttgtcctg 200
 tgcctactcg ggcttttctt ctccccgtgt ggagtggaag tttgaccaag 250
 gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
 gaggaccggg tgaccttctt gccaactggt atcaccttca agtccgtgac 350
 acgggaagac actgggacat acacttgtat ggtctctgag gaaggcggca 400
 acagctatgg ggaggtcaag gtcaagctca tcgtgcttgt gcctccatcc 450
 aagcctacag ttaacatccc ctcctctgcc accattggga accgggcagt 500
 gctgacatgc tcagaacaag atggttcccc accttctgaa tacacctggt 550
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 tcccctqtca gcctctgata ctggagaata cagctgtgag gcacggaatg 700
 ggtatgggac acccatgact tcaaatgctg tgcgcatgga agctgtggag 750
 cggaatgtgg gggtcatcgt ggcagccgtc cttgtaaccc tgattctcct 800
 gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg 850
 acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
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65 70 75 Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu 80 85 90

P1618P2C2 sequence listing.txt

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Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly
                                        100
 Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly 110 115 120
 Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro
125 130 135
                                                             135
 Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
                  140
 Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr
 Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
                                                             180
 Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly
 Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
 Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn
215 220 225
 Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe
                                                             255
 Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr
 Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala
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 Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
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<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 120
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<210> 121
<211> 50
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 121
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P1618P2C2 sequence listing.txt
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<223> Synthetic Oligonucleotide Probe
<400> 123
 taggaagagt tgctgaaggc acgg 24
<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 124
 ttgccttact caggtgctac 20
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<211> 20
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<220>
<223> Synthetic Oligonucleotide Probe
<400> 125
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<211> 1210
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<213> Homo Sapien
<400> 126
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 gctgctcggc ctcggactag gcctggaggc cgccgcgagc ccgctttcca 150
 ccccgacctc tgcccaggcc gcaggcccca gctcaggctc gtgcccaccc 200
 accaagttcc agtgccgcac cagtggctta tgcgtgcccc tcacctggcg 250
 ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
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ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc 350
ccctgcccct gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa 400
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cgctgagcga tgactgcatt ccactcacgt ggcgctgcga cggccaccca 500
gactgtcccg actccagcga cgagctcggc tgtggaacca atgagatcct 550
cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600
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<211> 282

<212> PRT

<213> Homo Sapien

<400> 127

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Leu Glu Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln 35 40 45

Ala Ala Gly Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln 50 55 60

Cys Arg Thr Ser Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp
65 70 75

Arg Asp Leu Asp Cys Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg 80 85 90

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P1618P2C2 sequence listing.txt
Ile Glu Pro Cys Thr Gln Lys Gly Gln Cys Pro Pro Pro Gly
Leu Pro Cys Pro Cys Thr Gly Val Ser Asp Cys Ser Gly Gly Thr
110 115 120
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Glu Leu Arg Cys Thr Leu Ser Asp Asp Cys Ile Pro Leu Thr Trp
140 145 150
Arg Cys Asp Gly His Pro Asp Cys Pro Asp Ser Ser Asp Glu Leu
                                      160
                                                            165
Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly Asp Ala Thr Thr
Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser Leu Arg Asn
                                                            195
                 185
Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Pro Ser
                                                            210
Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
230 235 240
                                                            240
Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala
Gln Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu
Ser Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
275 280
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<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 128
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<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 129
ttggttccac agccgagctc gtcg 24
<210> 130
<211> 50
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P1618P2C2 sequence listing.txt
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<213> Artificial Sequence
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<211> 1843
<212> DNA
<213> Homo Sapien
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<221> unsure
<222> 1837
<223> unknown base
<400> 131
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agctgcatgc atgagaccca cagactcttg caagctggat gccctctgtg 150
gatgaaagat gtatcatgga atgaacccga gcaatggaga tggatttcta 200
gagcagcagc agcagcagca gcaacctcag tcccccaga gactcttggc 250
cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300
cqqqcqqqtt cqatqacctt caaqtqtqtq ctgaccccgg cattcccgag 350
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 tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg aagatgctga 550
gattcataac aagacatata gacatggaga gaagctaatc atcacttgtc 600
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tgtcgcgatg atggaacgtg gaataatctg cccatctgtc aaggctgcct 700
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 cgctacaacc acggaactgt ggtggagttt tactgcgatc ctggctacag 1000
 cctcaccage gactacaagt acatcacctg ccagtatgga gagtggtttc 1050
 cttcttatca agtctactgc atcaaatcag agcaaacgtg gcccagcacc 1100
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ctcccaggtg ccaagagagc acccacctg cttcggacaa ccctgacata 1550
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tgcccactgg gtgttgtcc taagaaactg attgattaaa aaatttccca 1650
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cctttcctc tcttggttt agacaaatgt aaacaaagct ctgatcctta 1750
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<400> 132
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35
Gln Leu Thr Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro
50
Gly Ile Pro Glu Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe
65
Phe Glu Gly Ser Val Ala Arg Phe His Cys Gln Asp Gly Phe Lys
80

Leu Lys Gly Ala Thr Lys Arg Leu Cys Leu Lys His Phe Asn Gly 105

Thr Leu Gly Trp Ile Pro Ser Asp Asn Ser Ile Cys Val Gln Glu 115

Asp Cys Arg Ile Pro Gln Ile Glu Asp Ala Glu Ile His Asn Lys

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Thr	Tyr	Arg	His	Gly 140	Glu	Lys	Leu	Ile	11e 145	Thr	Cys	His	Glu	Gly 150
Phe	Lys	Ile	Arg	Tyr 155	Pro	Asp	Leu	His	Asn 160	Met	∨al	Ser	Leu	Cys 165
Arg	Asp	Asp	Glу	Thr 170	Trp	Asn	Asn	Leu	Pro 175	Ile	Cys	Gln	Gly	Cys 180
Leu	Arg	Pro	Leu	Ala 185	Ser	Ser	Asn	Gly	Tyr 190	val	Asn	Ile	ser	Glu 195
Leu	Gln	Thr	Ser	Phe 200	Pro	٧a٦	Gly	Thr	va1 205	Ile	Ser	Tyr	Arg	Cys 210
Phe	Pro	Gly	Phe	Lys 215	Leu	Asp	Gly	Ser	Ala 220	Tyr	Leu	Glu	Cys	Leu 225
Gln	Asn	Leu	Ile	Trp 230	Ser	ser	Ser	Pro	Pro 235	Arg	Cys	Leu	Ala	Leu 240
Glu	Ala	Gln	val	Cys 245	Pro	Leu	Pro	Pro	Met 250	val	Ser	His	Gly	Asp 255
Phe	∨al	Cys	His	Pro 260	Arg	Pro	Cys	Glu	Arg 265	Tyr	Asn	His	Gly	Thr 270
٧a٦	۷al	Glu	Phe	Tyr 275	Cys	Asp	Pro	Gly	Tyr 280	Ser	Leu	Thr	Ser	Asp 285
Tyr	Lys	Tyr	Ile	Thr 290	Cys	Gln	туr	Gly	G] u 295	Trp	Phe	Pro	Ser	Tyr 300
Gln	٧a٦	Tyr	Cys	11e 305	Lys	Ser	Glu	Gln	Thr 310	Trp	Pro	Ser	Thr	His 315
Glu	Thr	Leu	Leu	Thr 320	Thr	Trp	Lys	Ile	Va1 325	Ala	Phe	Thr	Ala	Thr 330
Ser	٧a٦	Leu	Leu	Va1 335	Leu	Leu	Leu	٧al	11e 340	Leu	Ala	Arg	Met	Phe 345
Gln	Thr	Lys	Phe	Lys 350	Ala	His	Phe	Pro	Pro 355	Arg	Glу	Pro	Pro	Arg 360
Ser	Ser	Ser	Ser	Asp 365	Pro	Asp	Phe	va1	Val 370	٧a٦	Asp	Gly	val	Pro 375
Val	Met	Leu	Pro	ser 380	Tyr	Asp	Glu	Ala		Ser	Glу	Gly	Leu	
Ala	Leu	Gly	Pro	G]y 395	туг	Met	Αla	Ser	val 400	Glу	Gln	Gly	Cys	Pro 405
Leu	Pro	۷al	Asp	Asp 410	Gln	Ser	Pro	Pro	Ala 415	туг	Pro	Gly	Ser	G]y 420
Asp	Thr	Asp	Thr	Gly 425	Pro	Gly	Glu	Ser	G1u 430	Thr	Cys	Asp	Ser	Va1 435
Ser	Gly	Ser	Ser	G]u 440	Leu	Leu	Gln	Ser	445	Tyr age 8		Pro	Pro	Arg 450

# P1618P2C2 sequence listing.txt Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile Ile 455 460 465

Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn 485 490

- <210> 133
- <211> 23
- <212> DNA
- <213> Artificial Sequence

<220>

- <223> Synthetic Oligonucleotide Probe
- <400> 133

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- <210> 134
- <211> 23
- <212> DNA
- <213> Artificial Sequence

<220>

- <223> Synthetic Oligonucleotide Probe
- <400> 134

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- <210> 135
- <211> 50
- <212> DNA
- <213> Artificial Sequence

<220>

- <223> Synthetic Oligonucleotide Probe
- <400> 135

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- <210> 136
- <211> 1815
- <212> DNA
- <213> Homo Sapien

<400> 136

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cccgccagcc cgctccaccg ccgtagcgcc cgagtgtcgg ggggcgcacc 150

cgaqtcqqqc catqagqccg ggaaccgcgc tacaggccgt gctgctggcc 200

gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc tgagtgcctc 250

ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

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<sup>&</sup>lt;210> 137

<sup>&</sup>lt;211> 382

<sup>&</sup>lt;212> PRT

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65 70 75 Gly Gln Leu Val Ser Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile 80 85 90 Glu Lys Phe Ile Glu Asn Leu Leu Pro Ser Asp Gly Asp Phe Trp 95 100 105 Ile Gly Leu Arg Arg Glu Glu Lys Gln Ser Asn Ser Thr Ala 110 115 120 Cys Gln Asp Leu Tyr Ala Trp Thr Asp Gly Ser Ile Ser Gln Phe 125 130 135 Arg Asn Trp Tyr Val Asp Glu Pro Ser Cys Gly Ser Glu Val Cys 140 145 Val Val Met Tyr His Gln Pro Ser Ala Pro Ala Gly Ile Gly Gly
155 160 165 Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys Asn Met Lys Asn 170 175 180 Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala Val Pro Ser 185 190 195 Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys Glu 215 220 225 Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser 230 235 240 230 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys 250 Val Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro 260 265 Thr Lys Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu 290 295 300

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P1618P2C2 sequence listing.txt
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 Leu Val Ser Val Glu Ser Gly Phe Val Thr Asn Asp Ile Tyr Glu
 Phe Ser Pro Asp Gln Met Gly Arg Ser Lys Glu Ser Gly Trp Val
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<400> 139
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<212> DNA
<213> Homo Sapien
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 ccccggcgcc cgcagaagac ttgtgtttgc ctcctgcagc ctcaacccgg 150
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<sup>&</sup>lt;210> 142

<sup>&</sup>lt;211> 428

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

<sup>&</sup>lt;400> 142
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Page 87

P1618P2C2 sequence listing.txt . 1 Val Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala 20 25 30 Leu Ala Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg
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P1618P2C2 sequence listing.txt
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Gly Ile Phe Asp His Lys Trp Pro Pro Phe Ala Val Asp Leu Thr
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Met Glu Leu Tyr Gln His Leu Glu Ser Lys Glu Trp Phe Val Gln
365 370 375
Leu Tyr Tyr His Gly Lys Glu Gln Val Pro Arg Gly Cys Pro Asp
Gly Leu Cys Pro Leu Asp Met Phe Leu Asn Ala Met Ser Val Tyr
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425
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<223> Synthetic Oligonucleotide Probe
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50 55 60 Leu Cys Arg Glu Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser
65 70 75 Gly Ile Leu Tyr Glu Pro Pro Ala Glu Lys Glu Gln Lys Val Leu 80 85 90 Ile Gln Ser Val Ser Cys Thr Gly Thr Glu Asp Thr Leu Ala Gln 95 100 105 Cys Glu Gln Glu Glu Val Tyr Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu Ser Ser Phe Ser Pro Val 125 130 Glu Gly Val Arg Leu Ala Asp Gly Pro Gly His Cys Lys Gly Arg 140 145 150 Val Glu Val Lys His Gln Asn Gln Trp Tyr Thr Val Cys Gln Thr 155 160 165 Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys Arg Gln Leu Gly 170 175 180 Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn Lys His Ala 185 190 195 Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys Ser Gly 200 205 210

<sup>&</sup>lt;210> 148

<sup>&</sup>lt;211> 347

<sup>&</sup>lt;212> PRT

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Asp Asn Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu
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Gly Cys Gly Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys 290 295 300
Tyr Gly Pro Gly Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys
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Ser Val
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200 205 210 Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr Ile 215 220 225 His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg 230 235 240 Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val 245 250 255 Glu Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys 260 265 270 Asp Val Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Page 94

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#### aaaaaaaaa a 1771

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P1618P2C2 seguence listing.txt
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### tattatata aaaagtaaaa aaaaaa 2076

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P1618P2C2 sequence listing.txt
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Ala Phe Glu Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser 290 295
Asp Pro Ser Tyr Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr
305 310
Asn Phe Leu Arg Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val
320 325 330
Lys Phe Leu Ser Leu Pro Glu Val Arg Gln Ala Ile His Val Gly
335 340 345
Asn Gln Thr Phe Asn Asp Gly Thr Ile Val Glu Lys Tyr Leu Arg
350 355 360
Glu Asp Thr Val Gln Ser Val Lys Pro Trp Leu Thr Glu Ile Met 365 370
Asn Asn Tyr Lys Val Leu Ile Tyr Asn Gly Gln Leu Asp Ile Ile
380 385
Val Ala Ala Ala Leu Thr Glu Arg Ser Leu Met Gly Met Asp Trp
395 400 405
Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys Lys Val Trp Lys
410 415 420
 Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile Arg Gln Ala
425 430 435
 Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His Ile Leu
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#### ttaagaaggt acatctgcaa aagcaaa 2477

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65 70 75 Ser Val Val Trp Val Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His Ser Glu Asn Arg Asp Trp Thr Phe Asn 95 100 105 His Leu Thr Val His Gln Gly Thr Gly Ala Val Tyr Val Gly Ala 110 115 120 Ile Asn Arg Val Tyr Lys Leu Thr Gly Asn Leu Thr Ile Gln Val 125 130 135 Ala His Lys Thr Gly Pro Glu Glu Asp Asn Lys Ser Arg Tyr Pro 140 145 150 Pro Leu Ile Val Gln Pro Cys Ser Glu Val Leu Thr Leu Thr Asn 155 Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser Glu Asn Arg Leu 170 175 180 Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys Leu Leu Arg 185 190 Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys Lys Glu 210 200 His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly 215 220 Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr 230 235 240 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg 245 250 255 250 Lys Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu 260 265 270

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P1618P2C2 sequence listing.txt
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Phe Ala Ser Gly Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu
305 310 315
Thr Pro Glu Gly Val Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr
320 325 330
Thr Ser Arg Ile Val Arg Leu Cys Lys Asp Asp Pro Lys Phe His 345
Ser Tyr Val Ser Leu Pro Phe Gly Cys Thr Arg Ala Gly Val Glu
350 355 360
Tyr Arg Leu Leu Gln Ala Ala Tyr Leu Ala Lys Pro Gly Asp Ser
365 370 375
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380 385
Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr His His Pro Pro Asp
395 400 405
 Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala Ile Asn Leu Gln
410 415 420
 Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu Gly Asn Leu
425 430 435
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440 445 450
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485 490 495
 Gly Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys
500 505 510
 Lys Val Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu
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Pro Pro Asp Leu Leu Pro Lys Met Pro Tyr Glu Pro Leu Thr Pro 385 390 Page 109
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P1618P2C2 sequence listing.txt

Page 112

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Cys	Pro	o Ar	g Gly	/ Pro 395	o Ile	e His	s Sei	r Ile	400	ı Pro	Met	: Thi	Phe	405
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Ile	Ser	Lys	Ser	туг 290	Leu	Glu	Αla	Phe	Asn 295	Ser	Asn	Gly	Asn	Asn 300
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Ile	е Ту	r Il	e Thr	G] (	u Ası O	o Asp	va <sup>-</sup>	i Ile	e Gli 38	n Ser 5	· Glr	n Asr	ı Ala	1 Leu 390
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Τh	r Le	u Ph	e va	1 G1 42	n Va 5	1 Se	r Le	u Hi	s Th 43	r se	r ASI	p Pr	0 A5	n Leu 435
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G٦	u Th	ır Cy	s Ly	s Va 47	ı1 Ту ′0	r Pr	o Le	u Ph	ne GT 47	у ні '5	s Ty	r Gl	y Ar	g Phe 480
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Trp Tyr Trp Gln Lys Glu Lys Ile Pro Lys Tyr Val Glu Phe Met 80 85 90

Lys Asp Asn Tyr Pro Pro Ser Phe Lys Tyr Glu Asp Phe Gly Pro 95 100 105

Leu Phe Thr Ala Lys Phe Phe Asn Ala Asn Gln Trp Ala Asp Ile 110 115

Phe Gln Ala Ser Gly Ala Lys Tyr Ile Val Leu Thr Ser Lys His Page 125

				125		Р1	618P	2C2	sequ 130	ence	lis	ting	.txt	135
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Tyr	ser	Leu	Phe	Glu 185	Trp	Phe	His	Pro	Leu 190	Phe	Leu	Glu	Asp	Glu 195
Ser	Ser	Ser	Phe	ніs 200	Lys	Arg	Gln	Phe	Pro 205	٧a٦	ser	Lys	Thr	Leu 210
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Trp	Ser	Asp	Glу	Asp 230	Glу	Gly	Ala	Pro	Asp 235	Gln	туг	Trp	Asn	Ser 240
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Lys	va1	Asn	Gly	Glu 365	Ala	ıle	Tyr	GTu	Thr 370	⊤yr )	Thr	Trp	Arg	Ser 375
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Lys	s Glu	ı Lys	Leu	val 395	Tyr	· Ala	ıle	Phe	400	Lys )	Trp	Pro	Thr	Ser 405
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Ile Val Phe Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly Pro Page 132

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Gly Val Lys Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr 50 55 60

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Pro Ala Leu Val Ser Pro Arg Arg Val Arg Val Lys Trp Trp Lys 80 85 90

P1618P2C2 sequence listing.txt Leu Ser Glu Asn Gly Ala Pro Glu Lys Asp Val Leu Val Ala Ile 95 Gly Leu Arg His Arg Ser Phe Gly Asp Tyr Gln Gly Arg Val His 110 115 120 120 Leu Arg Gln Asp Lys Glu His Asp Val Ser Leu Glu Ile Gln Asp 125 130 135 Leu Arg Leu Glu Asp Tyr Gly Arg Tyr Arg Cys Glu Val Ile Asp 140 145 150 Gly Leu Glu Asp Glu Ser Gly Leu Val Glu Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg Tyr Gln Phe Asn 170 175 180 Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala Ala Val Val 185 190 195 195 Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly Leu Asp 200 205 210 Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr Pro 215 220 225 Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro 230 235 240 Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr 245 250 255 Asp Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr 260 265 270 Leu Glu His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala 275 280 285 Cys Gln Glu Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe 290 295 300 Ala Ala Trp Lys Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp 305 310 315 Leu Ala Asp Gly Ser Val Arg Tyr Pro Val Val His Pro His Pro 320 325 330 Asn Cys Gly Pro Pro Glu Pro Gly Val Arg Ser Phe Gly Phe Pro 335 340 345 Asp Pro Gln Ser Arg Leu Tyr Gly Val Tyr Cys Tyr Arg Gln His 350 355 <210> 214 <211> 18 <212> DNA <213> Artificial Sequence <223> Synthetic Oligonucleotide Probe <400> 214

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130
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Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr Lys Val Gly 95 100

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Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr Ser 125 130 135

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Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln
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Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe  $50\,$ 

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Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu 125 130 135

Asn Lys Leu Arg Gln Leu Asn Leu Asn Glu Trp Thr Leu Asp 140 145 150

Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu 155 160 165 Page 157

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Trp	Leu	Tyr	His	Thr 215	Ala	Ala	Lys	Ile	Glu 220	Ala	Pro	Ala	Leu	Ala 225
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Arg	Leu	Lys	Ser	Asn 290	Leu	Ser	Lys	Leu	Pro 295	Gln	٧a٦	val	Thr	Asp 300
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Ile	Phe	ser	Leu	His 350	Asn	Leu	Gln	Glu	11e 355	Asp	Leu	Lys	Asp	Asn 360
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Arg	g Lys	s Lei	ı Arg	1 Tyr 425	Leu	ı Asp	Lei	ı Ser	нis 430	Asn	Asn	Leu	Thr	• Phe 435
Lei	ı Pro	o Ala	a Asp	1]6 440	e Gly	/ Leu	ı Lei	u Glr	1 Asn 445	Leu	Glm	Asr	Leu	450
Ile	e Thi	r Ala	a Asr	1 Arc	ıle 5	e Glu	u Thi	r Lei	460	Pro	Glu	ı Let	ı Phe	e Gln 465
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Leu	Ala	Phe	Tyr	Trp 425	Ile	Leu	Lys	Ala	Gly 430	His	Met	٧al	Pro	Ser 435
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  Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
110 115
  Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
125 130 135
  Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr
140 145
  Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
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Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val 255

Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val 270

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40
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215 220 225 Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu Ala Gin Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly
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Lys Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp
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Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg
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Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser 410 415 420
Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His
                  425
                                        430
                                                              435
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440 445 450
                                                              450
Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg
                  455
Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
470 475 480
                                                              480
Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser
Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln
                                        505
                                                               510
                  500
His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
515 520
                                                               525
Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro
530 535 540
                  530
Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu
                                                               555
                  545
                                        550
Cys
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<sup>&</sup>lt;210> 260

<sup>&</sup>lt;211> 1638

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo Sapien

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cgcggcccgg	gcgggctgct	cggcgcggaa	cagtgctcgg	catggcaggg	100
attccagggc	tcctcttcct	tctcttcttt	ctgctctgtg	ctgttgggca	150
agtgagccct	tacagtgccc	cctggaaacc	cacttggcct	gcataccgcc	200
tccctgtcgt	cttgccccag	tctaccctca	atttagccaa	gccagacttt	250
ggagccgaag	ccaaattaga	agtatcttct	tcatgtggac	cccagtgtca	300
taagggaact	ccactgccca	cttacgaaga	ggccaagcaa	tatctgtctt	350
atgaaacgct	ctatgccaat	ggcagccgca	cagagacgca	ggtgggcatc	400
tacatcctca	gcagtagtgg	agatggggcc	caacaccgag	actcagggtc	450
ttcaggaaag	tctcgaagga	agcggcagat	ttatggctat	gacagcaggt	500
tcagcatttt	tgggaaggac	ttcctgctca	actacccttt	ctcaacatca	550
gtgaagttat	ccacgggctg	caccggcacc	ctggtggcag	agaagcatgt	600
cctcacagct	gcccactgca	tacacgatgg.	aaaaacctat	gtgaaaggaa	650
cccagaagct	tcgagtgggc	ttcctaaagc	ccaagtttaa	agatggtggt	700
cgaggggcca	acgactccac	ttcagccatg	cccgagcaga	tgaaatttca	750
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atgccaatga	catcggcatg	gattatgatt	atgccctcct	ggaactcaaa	850
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caggcaattt	ggtgtatcgc	ttctgtgacg	tcaaagacga	gacctatgac	1000
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ttggcatttt	ttcagggcac	cagtgggtgg	acatgaatgg	ttccccacag	1150
gatttcaacg	tggctgtcag	aatcactcct	ctcaaatatg	cccagatttg	1200
ctattggatt	aaaggaaact	acctggattg	tagggagggg	tgacacagtg	1250
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tgtgtgtaag	gtgtcttata	atcttttacc	tatttcttac	aattgcaaga	1400
			•	tcatatatca	
				aaaatactga	
tttggggcaa	tgaggaatat	ttgacaatta	agttaatctt Page 1	cacgtttttg 68	1550

caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600 atatttggca tacaagagat atgaaaaaaa aaaaaaaa 1638

- <210> 261
- <211> 383
- <212> PRT
- <213> Homo Sapien

#### <400> 261

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- Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro 20 25 30
- Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr 35 40 45
- Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
  50 55 60
- Val Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu 65 70 75
- Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu 80 85 90
- Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile 95 100 105
- Leu Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser 110 115 120
- Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser 125 130 135
- Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe 140 145 150
- Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val 155 160 165
- Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
  170 175 180
- Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu 185 190 195
- Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr 200 205 210
- Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys 215 220 225
- Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp 230 235 240
- Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro 245 250 255
- His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Page 169

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P1618P2C2 sequence listing.txt 265
                  260
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
275 280 285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp 290 295
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
305 310 315
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln 320 325 330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp 335 340 345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
350 355 360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly 365 370 375
Asn Tyr Leu Asp Cys Arg Glu Gly 380
<210> 262
<211> 1378
<212> DNA
<213> Homo Sapien
<400> 262
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accttcacct ccctgctgct gctggcgtcg acagccatcc tcaatgcggc 150
caggatacct gttcccccag cctgtgggaa gccccagcag ctgaaccggg 200
ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300
ctgggtgatc actgctcc actgtttcaa ggacaacctg aacaaaccat 350
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
cggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450
ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500
ccatacagtt ctcagagcgg gtcctgccca tctgcctacc tgatgcctct 550
atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650
ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700
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ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800

Page 170

tggacggcg ctggctgcg gccggcatca tcagctggg cgagggctgt 850 gccgaggcgca acaggcccgg ggtctacatc agcctctcg cgcaccgctc 900 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050 cacatctgga tctggatctg cggcggctc gggcggtttc ccccgccgta 1100 aataggctca tctacctcta cctctggggg cccggacggc tgctgcggaa 1150 aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200 catcaggccc cgcccaacgg cttttgtgta tataaatgtt aatgatttt 1300 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350 ataaattatt tattctccaa aaaaaaaa 1378

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<210> 263
<211> 317
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<212> PRT

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Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu 30

Asn Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln 45

Gln Leu Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu 60

Trp Pro Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys 75

Ala Gly Ser Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His 90

Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly 155

Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys 120

Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys 135

Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala 165

<sup>&</sup>lt;213> Homo Sapien

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Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp
170 175 180
Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
185 190 195
Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
200 205 210
Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met 215 220
Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
230 235 240
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu 245 250 255
Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
260 265 270
Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
275 280 285
                                                                285
Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
290 295 300
Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala 305 310
Arg Ser
<210> 264
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 264
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<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 265
 gcagaggtgt ctaaggttg 19
<210> 266
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
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<400> 266
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<400> 267
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<400> 268
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<210> 269
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<213> Artificial Sequence
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<400> 269
gaatgccctg caagcatcaa ctgg 24
<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 270
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<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 271
gcggaagggc agaatgggac tccaag 26
<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence
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<220>
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<400> 272
cagccctgcc acatgtgc 18
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<223> Synthetic Oligonucleotide Probe
<400> 273
 tactgggtgg tcagcaac 18
<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 274
 ggcgaagagc agggtgagac cccg 24
<210> 275
<211> 45
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<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 275
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<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
 <223> Synthetic Oligonucleotide Probe
<400> 276
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 <210> 277
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic Oligonucleotide Probe
 <400> 277
  ggctatgaca gcaggttc 18
 <210> 278
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P1618P2C2 sequence listing.txt
<211> 18
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 278
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<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
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<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 280
 ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45
<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence
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<400> 281
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<210> 282
<211> 61
 <212> DNA
 <213> Artificial Sequence
 <223> Synthetic Oligonucleotide Probe
 <400> 282
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 tgccaggtgg a 61
<210> 283
<211> 119
<212> DNA
 <213> Artificial Sequence
 <223> Synthetic Oligonucleotide Probe
                                         Page 175
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<400> 283 ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50 gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100 atgctgtgtg ccggctact 119 <210> 284 <211> 1875 <212> DNA <213> Homo Sapien <400> 284 gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50 ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100 agatgaggag aaacgtttga tggtggagct gcacaacctc taccgggccc 150 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250 caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350 tacaacctca gcgccgccac ctgcagccca ggccagatgt gcggccacta 400 cacgcaggtg gtatgggcca agacagagag gatcggctgt ggttcccact 450 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550 ' ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600 tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700 aatgggtact ccttcttccc tagcaacggg gattccggct ttcttggtaa 750 cagaggtete aggeteetg geaaceaagg etetgeetge tgtggaaace 800 caggccccaa cttccttagc aacgaaagac ccgccctcca tggcaacaga 850 ggctccacct tgcgtaacaa ctgaggtccc ttccattttg gcagctcaca 900 gcctgccctc cttggatgag gagccagtta ccttccccaa atcgacccat 950 gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050 caagggaact cctaccccat gcccaggagg aggctgaggc tgaggctgag 1100 ttgcctcctt ccagtgaggt cttggcctca gtttttccag cccaggacaa 1150 gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200 agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250

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gggcgtgccc tggctctgca gtcgtccttg ccaggtgcag agggccctga 1300 caagcctagc gttgtgtcag ggctgaactc gggccctggt catgtgtggg 1350 gccctctcct gggactactg ctcctgcctc ctctggtgtt ggctggaatc 1400 ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450 catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500 ggccctccgg aagggaaagg ctacgggca tgtgcctcat cacaccatcc 1550 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600 ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650 ggggtgggag gattgaggg agctcactgc ctacctggcc tggggctgc 1700 tgcccacaca gcatgtgcgc tctccctgag tgcctgtaa gctggggatg 1750 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800 tgagtggggg aggcagggac gagggaagga aagtaactcc tgactctca 1850 ataaaaacct gtccaacctg tgaaa 1875
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<210> 285
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# 

<sup>&</sup>lt;211> 463

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

P1618P2C2 sequence listing.txt Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly 170 180 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser 185 190 195 185 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro 200 205 210 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser 215 . 220 225 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile 230 235 240 Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr 245 250 245 Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr 275 280 285 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu 300 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile 305 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser 320 325 330 330 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu 350 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro 370 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr 385 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser 405 395 400 Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser 420 410 Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser 425 430 435 Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
440 445 450 Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe 460 455

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<211> 24
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<220>
<223> Synthetic Oligonucleotide Probe
<400> 287
ctcatattgc acaccagtaa ttcg 24
<210> 288
<211> 45
<212> DNA
<213> Artificial Sequence
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<400> 288
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<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien
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caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200
acaacaatga attggagacc attccaaatc tgggaccagt ctcggcaaat 250
attacacttc tctccttggc tggaaacagg attgttgaaa tactccctga 300
acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350
atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450
tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500
ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550
aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600
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Leu	Lys	Thr	Leu	Asp 305	Leu	Lys	Asn	Asn	G]u 310		Ser	Trp	Thr	Ile 315
Glu	Asp	Met	Asn	Gly 320	Ala	Phe	Ser	Gly	Leu 325	Asp	Lys	Leu	Arg	Arg 330
Leu	Ile	Leu	Gln	Gly 335	Asn	Arg	Ile	Arg	Ser 340	Ile	Thr	Lys	Lys	Ala 345
Phe	Thr	Gly	Leu	Asp 350	Ala	Leu	Glu	His	Leu 355	Asp	Leu	Ser	Asp	Asn 360
Ala	Ile	Met	Ser	Leu 365	Gln	Gly	Asn	Ala	Phe 370	Ser	Gln	Met	Lys	Lys 375
Leu	Gln	Gln	Leu	His 380	Leu	Asn	Thr	Ser	Ser 385	Leu	Leu	Cys	Asp	Cys 390
Gln	Leu	Lys	Trp	Leu 395	Pro	Gln	Trp	٧a٦	А]а 400	Glu	Asn	Asn	Phe	Gln 405
Ser	Phe	۷al	Asn	Ala 410	Ser	Cys	Ala	His	Pro 415	Gln	Leu	Leu	Lys	Gly 420
Arg	Ser	Ile	Phe	Ala 425	۷al	Ser	Pro	Asp	G]y 430	Phe	۷a٦	Cys	Asp	Asp 435
Phe	Pro	Lys	Pro	G1n 440	Ile	Thr	۷al	Gln	Pro 445	Glu	Thr	Gln	Ser	Ala 450
Ile	Lys	Gly	Ser	Asn 455	Leu	Ser	Phe	Ile	Cys 460	Ser	Ala	Ala	Ser	Ser 465
Ser	Asp	Ser	Pro	Met 470	Thr	Phe	Ala	Тгр	Lys 475	Lys	Asp	Asn	Glu	Leu 480
Leu	His	Asp	Ala	G]u 485	Met	Glu	Asn	Tyr	Ala 490	His	Leu	Arg	Ala	Gln 495
Gly	Gly	Glu	۷al	Met 5 <b>0</b> 0	Glu	Tyr	Thr	Thr	11e 505	Leu	Arg	Leu	Arg	Glu 510
			Ala	515					520	-			Ser	525
His	Phe	Gly	Ser	Ser 530	Tyr	Ser	val	Lys	Ala 535	Lys	Leu	Thr	Val	Asn 540
Met	Leu	Pro	Ser	Phe 545	Thr	Lys	Thr	Pro	Met 550	Asp	Leu	Thr	Ile	
Ala	Gly	Ala	Met	Ala 560	Arg	Leu	Glu	Cys	Ala 565	Ala	۷a٦	Gly	His	Pro 570
Ala	Pro	Gln	Ile	Ala 575	Trp	Gln	Lys	Asp	Gly 580	Gly	Thr	Asp	Phe	Pro 585
Ala	Ala	Arg	Glu	Arg 590	Arg	Met	His	val	Met 595	Pro	Glu	Asp	Asp	va1 600
Phe	Phe	Ile	Val	Asp 605	Val	Lys	Ile	Glu	610	Ile e 18	_	Val	Tyr	Ser 615

Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu G G G G G G G G G G G G G G G G G G G															
Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile 76 Gly Gly Ser Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp 8 Gly Glu His Phe Phe Ala Ala Gly Asn Gen Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys 7 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val Ile Ile Ala Val Cys Cys Val Val Gly Thr Ser Leu Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val Ile Ile Tyr His Thr Arg Arg Arg Arg Asn Glu Asp Cys Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Asp Asp Gly Try Val Ser Ser Gly Ala Gly Ser Gly Ser His His Gln Phe Val Thr Ser Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr Gly Ser Fro Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr Gly Cys Gly Asp Ser Fro Gly Fro Phe Glu Thr Tyr His Thr Arg Asp Val Gly Thr Ser Cys Rep Gly Ala Gly Thr Ser Gly Ser His His Gln Phe Val Thr Ser Cys His Ile Asp Asp Ser Ser Gly Ala Gly Phe Phe Leu Gly Ser Thr Gly Pro Met Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His Rep Glu Pro Ser Gly Asp Pro Arg Thr Val Leu Met Asp His Tyr Gly Cys Gly Cys Tyr Pro Cys Ser His Glu Pro Ser Glu Glu Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser Cys Glu Arg Ser Pro Phe Ser Asn Ile Ser Tyr Gly Ser	Cys	s Thi	r Ala	a Glr	620	ser )	^ Ala	a Gly	/ Sei	11e 625	Sei	^ Ala	a Ası	n Ala	a Thr 630
Gly Gly Ser Pro Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp & Asp	Lei	ı Thi	^ ∨a⁻	l Leu	Glu 635	Thr	Pro	Ser	Phe	e Leu 640	ı Arg	) Pro	) Lei	ı Leı	Asp 645
Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Ge 688  Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys 7695  Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn 7705  Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln M 7715  Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Y 740  Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Y 755  Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp C 770  Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile P 785  Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp G 880  Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr Ser Gly Thr Ser Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Val Glu Ala Ala Thr Ser Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Val Glu Ala Ala Thr Ser Ser Gly Ala Gly Phe Phe Leu Gly Ser Thr Gly Pro Met Ty 886  Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Ty 887  Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Ty Gly Pro Ser Glu Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His Rep Glu Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Flat Arg Ser Phe Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Flat Arg Ser Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Flat Arg Ser Pro Phe Ser Asn Ile Ser Ty Gly Pro Ser Glu Glu Flat Arg Ser Pro Phe Ser Asn Ile Ser Ty Gly Flat Arg Ser Pro Phe Ser Asn Ile Ser Typ Gly Flat Arg Phe Phe Ser Asn Ile Ser Typ Gly Flat Arg Phe Phe Cys Flat Arg Phe Phe Ser Asn Ile Ser Typ Gly Flat Arg Phe Phe Phe Leu Cys Gly Arg Phe Phe Phe Phe	Arg	g Thr	' Val	l Thr	650	Gly	/ Glu	Thr	· Ala	val 655	Leu	ı G]r	ı Cys	ıle	Ala 660
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Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn y 710 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln M 725 Pro Thr Pro Thr Cys Asp Ser Pro Gln M 740 Asp Asp Asp Asp Gly Trp Ala Thr Val Gly Y 745 Val Ile Ile Ala Val Cys Cys Val Val Gly Thr Ser Leu M 755 Val Cys Cys Val Val Gly Thr Ser Leu M 755 Val Val Cys Cys Val Val Gly Thr Ser Leu M 755 Val Val Val Gly Thr Ser Leu M 755 Val Val Val Gly Thr Ser Leu M 755 Val Val Val Gly Thr Ser Leu M 755 Val Val Val Gly Thr Ser Leu M 760 Asp Asp Asp Glu Asp M 755 Asp Glu Thr Asn Leu M 756 Asp Asp Glu Asp M 756 Asp Glu Thr Ash Leu M 756 Asp Asp Asp Glu Asp M 756 Asp M	Pro	Leu	ı Val	Val	Thr 680	Glu	ı Arg	His	Phe	Phe 685	Ala	аЛа	ı Gly	⁄ Asn	G]n 690
Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln M 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Leu	ı Leu	ıle	: Ile	Val 695	Asp	Ser	Asp	Val	Ser 700	Asp	Ala	Gly	Lys	Tyr 705
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Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Asp Arg Gln Asp Glu Tyr Val Ser Ser Glu Ser Gly Ser His His Asp Ser Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Ala Ala Ala Thr Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Ty Res Asp Leu Phe Leu Cys Asp Pro Phe Leu Gly Ser Thr Gly Pro Met Ty Res Asp Cys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His Asp Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Ty Gly Pro Ser Glu Glu Glu Ser Tyr Gly Ser Asp Pro Cys Ser His Ty Gly Pro Ser Glu Glu Glu Ser Tyr Gly Ser Asp Pro Cys Ser His Ty Gly Pro Ser Glu Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trg Gly Ser Glu Glu Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trg Gly Ser Glu Glu Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trg Gly Ser Tyr Pro Cys Ser Tyr Gly Ser Glu Glu Arg Ser Phe Ser Asn Ile Ser Trg Gly Ser Glu Glu Arg Ser Phe Ser Asn Ile Ser Trg Gly Ser Tyr Gly Ser Asn Ile Ser Trg Gly Ser Glu Arg Ser Phe Ser Asn Ile Ser Trg Gly Ser Asn Ile Ser Trg Gly Ser Asn Glu Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trg Gly Ser Asn Glu Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trg Gly Ser Asn Glu Glu Glu Glu Glu Glu Glu Glu Arg Ser Phe Ser Asn Ile Ser Trg Gly Glu	∨al	Ile	Ile	Ala	Va] 755	val	Cys	Cys	۷al	Val 760	Gly	Thr	Ser	Leu	va1 765
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Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly The Reservation of the Reservatio	Ser	Tyr	Leu	Ser	Ser 800	Gln	Gly	Thr	Leu	Ala 805	Asp	Arg	Gln	Asp	Gly 810
Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala The 845  Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Ty 860  Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His 880  Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Ty 890  Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His 910  Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Tr 930	Tyr	٧a٦	Ser	Ser	Glu 815	Ser	Gly	Ser	His	His 820	Gln	Phe	٧al	Thr	Ser 825
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Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr Hi 885  Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Ty 890  Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser Hi 910  Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Tr 920	Cys	His	Ile	Asp	As <b>n</b> 845	Ser	Ser	Glu	Ala	Asp 850	Val	Glu	Ala	Ala	Thr 855
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Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe 110 115 120

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				330	,				533	)				u Leu 540
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Phe	Phe	Ile	va1	Asp 665	Val	Lys	Ile	Glu	Asp 670	Ile	Gly	۷al	Tyr	Ser 675
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Leu <sup>-</sup>	Thr	Val	Leu	Glu 695	Thr	Pro	Ser	Phe	Leu 700	Arg	Pro	Leu	Leu	Asp 705
Arg -	Thr	Val	Thr	Lys 710	Gly	Glu	Thr	Аlа	Val 715	Leu	Gln	Cys	Ile	Ala 720
Gly (	3ly	Ser	Pro	Pro 725	Pro	Lys	Leu	Asn	Trp 730	Thr	Lys	Asp	Asp	Ser 735
Pro l	₋eu '	۷a٦	۷a٦	Thr 740	Glu .	Arg	His	Phe	Phe 745	Ala	Ala	Gly	Asn	G1n 750
Leu L	.eu :	Ile	Ile	Val 755	Asp	Ser	Asp	Val	Ser 760	Asp	Ala	Gly	Lys	Tyr 765
Thr (	:ys (	Glu	Met	Ser . 770	Asn '	Thr	Leu	Gly	Thr 775	Glu	Arg	Gly	Asn	
Arg L	.eu s	Ser	Val	Ile 785	Pro <sup>-</sup>	Thr	Pro	Thr	Cys 790	Asp	Ser	Pro	Gln	Met 795
Thr A	la F	Pro	Ser	Leu / 800	Asp A	Asp	Asp	Gly	Trp 805	Ala	Thr	val	Gly	
Val I	le 1	le /	41a	Val v 815	∕al d	Cys	Cys	Val	Val 820	Gly	Thr	Ser	Leu	
Trp V	al v	/al :	Ile	Ile 1 830	Γyr H	His '	Thr	Arg	835	Arg , e 19		Glu	Asp	Cys 840

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Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
                890
                                                         900
Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
                                                         915
Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
                                                         930
Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
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                                     940
                                                         945
Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
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                                                         990
Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
                995
                                    1000
                                                        1005
Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
               1010
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
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                                    1030
                                                        1035
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               1055
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                                                        1080
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                                    1090
               1085
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
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                                    1105
                                                        1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr
               1115
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<sup>&</sup>lt;211> 18

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Artificial Sequence

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<210> 297
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<212> DNA
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<223> Synthetic Oligonucleotide Probe
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 ggctggagac actgaacct 19
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<210> 299
<211> 22
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<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 299
 cattcccagt ataaaaattt tc 22
<210> 300
<211> 18
<212> DNA
<213> Artificial Sequence
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<211> 24
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<211> 50
<212> DNA
<213> Artificial Sequence
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<211> 28
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 303
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<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 304
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<210> 305
<211> 45
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 305
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<210> 306
<211> 24
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 306
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<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 307
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<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 308
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<210> 309
<211> 50
<212> DNA
<213> Artificial Sequence
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<400> 309
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<212> DNA
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agagaacgaa tttgcggagg aggagccggt gctggtactg agccctgagg 600
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  agctcagcca cacacaacta ccctccaaac caccacagtc tctgtcacac 2550
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P1618P2C2 sequence listing.txt
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<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien
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                                      Page 201
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P1618P2C2 sequence listing.txt tcaattggac tctcccaggt tccacagaac agtaatattt tttgaacaat 2650 aggtacaata gaaggtcttc tgtcatttaa cctggtaaag gcagggctgg 2700 agggggaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750 gtagatccat ttttaatggt tcatttcctt tatggtcata taactgcaca 2800 gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850 tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900 catcttgttt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950 tccaaatggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000 aat 3003 <210> 315 <211> 509 <212> PRT <213> Homo Sapien <400> 315 Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu 1 5 10 15 Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val 20 25 30 Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys 45 Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
50 55 60 Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
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		•												
Lys	Cys	ніѕ	Lys	G]y 200	Phe	P Asp	1618 Leu	P2C2 Met	seq Tyr 205	Ile	e li Gly	stin Gly	g.tx Lys	t Tyr 210
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Ser	Ser	Phe	Ala	Arg 230	Cys	Tyr	Asn	٧a٦	Arg 235	Gly	Ser	Tyr	Lys	Cys 240
Lys	Cys	Lys	Glu	Gly 245	Tyr	Gln	Gly	Asp	Gly 250	Leu	Thr	Cys	Val	Tyr 255
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Lys	Gly	Asn	Gly	Thr 275	Ile	Leu	Lys	Gly	Asp 280	Thr	Gly	Asn	Asn	Asn 285
Тгр	Ile	Pro	Asp	Va1 290	Gly	Ser	Thr	Trp	Trp 295	Pro	Pro	Lys	Thr	Pro 300
Tyr	Ile	Pro	Pro	Ile 305	Ile	Thr	Asn	Arg	Pro 310	Thr	Ser	Lys	Pro	Thr 315
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Thr	Asp	Pro	Gln	Lys 380	Pro	Arg	Gly	Asp	va1 385	Phe	Ser	۷al	Leu	Va1 390
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Lys	Asp	Asn	Asp	Leu 410	His	Trp	Glu	Pro	Ile 415	Arg	Asp	Pro	Ala	G]y 420
Gly	Gln	Tyr	Leu	Thr 425	٧a٦	Ser	Ala	Ala	Lys 430	Ala	Pro	Gly	Gly	Lys 435
Ala	Ala	Arg	Leu	Va1 440	Leu	Pro	Leu	Gly	Arg 445	Leu	Met	His	Ser	G]y 450
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Gly	Thr	Leu	Gln	va1 470	Phe	۷al	Arg	Lys	His 475	Glу	Ala	His	Gly	Ala 480
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50 55 60 Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
65 70 75 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro 80 85 90 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu 120 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr 125 130 135 130 135 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr 140 145 150 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg 165 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr 170 175 180 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala 195 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg 200 205 210 200 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile 220 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu 230 235 240 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu 245 255 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser

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Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp

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Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp
350 355 360
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Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe
395 400 405
                                                           405
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35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln 50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
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Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly Page 210

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 Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser 125 130
                                                            135
 Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150
 Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
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                                       160
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 Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
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170 175 180 Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln 190 Leu Asp Ala Gly Glu Glu Ala Thr Thr Lys Ser Gln Val Leu 210 Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg 215 220 225 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His 240 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu 245 250 255 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu 260 265 270 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro 285 Page 214

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35 40 45
Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
50 55 60
Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
65 70 75
Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
80 85 90
Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala
95 100 105
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Va	l Le	u Th	r Se	r Ar 11	g Ala 0	a Thi	P1618 r Leu	3P2C2 I Ser	? sec Thr 115	: Lei	e li LAla	isti Va	ng.t: l Ala	xt a Val 120
As	n Ar	g Th	r Va	12 12	а Нія 5	s His	s Phe	Pro	Arg 130	Leu	Leu	туі	r Phe	Thr 135
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Hi	s Gl	y As	p Gl	u Are 15	g Pro	Ala	l Trp	Leu	Met 160	Ser	Glu	Thr	. Ter	1 Arg 165
His	s Le	u Hi:	s Th	r His 170	5 Phe	e Gly	Ala	Asp	Tyr 175	Asp	Trp	Phe	Phe	11e 180
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Ala	a Gly	/ His	s Le	u Ser 200	lle	Asn	Gln	Asp	Leu 205	Tyr	Leu	Gly	Arg	Ala 210
Glu	ı Glu	ı Ph∈	e Ile	e Gly 215	Ala	Gly	Glu	Gln	Ala 220	Arg	Tyr	Cys	His	G]y 225
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Arg	Leu	His	Lys	Arg 320	Phe	Ser	Ala	Leu	G1u 325	Leu	Glu	Arg	Ala	Tyr 330
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Pro	Ala	Pro	Phe	Thr 365	Pro	His	Ser /	Arg i	Phe 9 370	Glu '	val	Leu	Gly	Trp 375
Asp	Tyr	Phe	Thr	Glu 380	Gln	His	Thr I	Phe s	Ser (	Cys /	4la /	Asp		Ala 390
Pro	Lys	Cys	Pro	Leu 395	Gln	Gly .	Ala s	Ser A	Arg / 400	Ala A	Asp '	√al (	Gly .	Asp 405
Ala	Leu	Glu	Thr	Ala 410	Leu •	Glu (	Gln L	₋eu A	Asn <i>A</i> 115	Arg A	Arg -	Tyr (		Pro 420
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Glu	Cys	٧a٦	Thr	Gln 455	Arg	GТу	His	Arg	Arg 460	Ala	Leu	Ala	Arg	Arg 465
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Pro	Tyr	Val	Thr	Glu 485	Ala	Thr	Arg	٧a٦	G]n 490	Leu	۷a٦	Leu	Pro	Leu 495
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Pro	Glu	∨al	Leu	Asn 605	Arg	Cys	Arg	Met	Asn 610	Ala	Ile	Ser	Gly	Trp 615
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Pro	Pro	Ser	Pro	Pro 650	Gly	Ala	Asp	Pro	ser 655	Arg	Gly	Ala	Pro	11e 660
Gly	Gly	Arg	Phe	Asp 665	Arg	Gln	Ala	Ser	Ala 670	Glu	GТу	Cys	Phe	Tyr 675
Asn	Ala	Asp	Tyr	Leu 680	Ala	Ala	Arg	Ala	Arg 685	Leu	Ala	Gly	Glu	Leu 690
Ala	Gly	Gln	Glu	G] u 695	Glu	Glu	Ala	Leu	G]u 700	Gly	Leu	Glu	Val	Met 705
Asp	val	Phe	Leu	Arg 710	Phe	Ser	Gly	Leu	His 715	Leu	Phe	Arg	Ala	Val 720
Glu	Pro	Gly	Leu	Val 725	Gln	Lys	Phe	Ser	Leu 730	Arg	Asp	Cys	Ser	Pro 735
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P1618P2C2 sequence listing.txt Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu 740 745 750 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu 755 760 765 Gln Glu Gln Ala Asn Ser Thr <210> 340 <211> 1572 <212> DNA <213> Homo Sapien <400> 340 cggagtggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50 tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400 gtttgagtca attaatatgg acacaaatga catgtggtta atgatgagaa 450 aagcttacaa atacgccttt gataagtata gagaccaata caactggttc 500 ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750 cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800

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<213> Homo Sapien

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Gly His Gly Asn Arg Met His His His Glu His His Leu Gln 35 40 45

Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg
50 55 60

Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val 65 70 75

Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp

Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val 95 100 105

Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu 110 115 120

Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp 125 130 135

Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile 140 145 150

Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln
155 160 165

Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr 170 175 180

Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys 185 190 195

Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln 200 205 210

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Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val
215 220 225
   Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
                     230
  Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile
245 250 255
  Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys
260 265 270
  Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
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P1618P2C2 sequence listing.txt
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<211> 48
<212> DNA
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<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
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<211> 47
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<223> Synthetic Oligonucleotide Probe
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<400> 366
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P1618P2C2 sequence listing.txt
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<211> 997
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tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200
atttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcatct 250
ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300
ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350
gaactgggaa tattttcaat ccagctgcta cttctttct actgacacca 400
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taaaatgaga_gagtttttta_ttggactgtc_agaccaggtt_gtcgagggtc_550
agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600
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gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700
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 Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro
 Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
65 70 75
 Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser
80 85 90
 Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
95 100 105
 Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser
 Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg
125 130 135
 Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp
140 145
 Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
155 160 165
 Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala
 Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
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<220>

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